

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: d'Apice, Anthony J.F.
Pearse, Martin J.
Rchins, Allan J.
Crawford, Robert J.
Rathjen, Peter D.

(ii) TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 120 South Sixth Street, Suite 2500
(C) CITY: Minneapolis
(D) STATE: MN
(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/378,617
(B) FILING DATE: 26-JAN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ellinger, Mark S.
(B) REGISTRATION NUMBER: 34,812
(C) REFERENCE/DOCKET NUMBER: 06868/005001

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAATTCAAG CCCTGCCTCC TTCTGCAG

28

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAATTCAAG GAGAAAATAA TGAATGTC

28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGAATTGGG GATCTGCCTT GTACCACC

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGAATTCGA AATCACTGGG AATTTACA

28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAATTCA G CATGATGCGC ATGAAGAC

28

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGAATTCT TTTTTTTTTT TVN

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCCCTGCCT CCTTCTGCAG AGCAGAGCTC ACTAGAACCTT GTTTCGCCCTT TTACTCTGGG

60

GGGAGAGAAG CAGAGGATGA GGAGAAAATA ATG AAT GTC AAA GGA AGA GTG GTT
Met Asn Val Lys Gly Arg Val Val
1 5

114

CTG TCA ATG CTG CTT GTC TCA ACT GTA ATG GTT GTG TTT TGG GAA TAC
Leu Ser Met Leu Leu Val Ser Thr Val Met Val Val Phe Trp Glu Tyr
10 15 20

162

ATC AAC AGC CCA GAA GGT TCT TTG TTC TGG ATA TAC CAG TCA AAA AAC
Ile Asn Ser Pro Glu Gly Ser Leu Phe Trp Ile Tyr Gln Ser Lys Asn
25 30 35 40

210

CCA GAA GTT GGC AGC AGT GCT CAG AGG GGC TGG TGG TTT CCG AGC TGG
Pro Glu Val Gly Ser Ser Ala Gln Arg Gly Trp Trp Phe Pro Ser Trp
45 50 55

258

TTT AAC AAT GGG ACT CAC AGT TAC CAC GAA GAA GAC GCT ATA GGC
Phe Asn Asn Gly Thr His Ser Tyr His Glu Glu Asp Ala Ile Gly
60 65 70

306

AAC GAA AAG GAA CAA AGA AAA GAA GAC AAC AGA GGA GAG CTT CCG CTA
Asn Glu Lys Glu Gln Arg Lys Glu Asp Asn Arg Gly Glu Leu Pro Leu
75 80 85

354

GTG GAC TGG TTT AAT CCT GAG AAA CGC CCA GAG GTC GTG ACC ATA ACC	402
Val Asp Trp Phe Asn Pro Glu Lys Arg Pro Glu Val Val Thr Ile Thr	
90 95 100	
AGA TGG AAG GCT CCA GTG GTA TGG GAA GGC ACT TAC AAC AGA GCC GTC	450
Arg Trp Lys Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Arg Ala Val	
105 110 115 120	
TTA GAT AAT TAT TAT GCC AAA CAG AAA ATT ACC GTG GGC TTG ACG GTT	498
Leu Asp Asn Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu Thr Val	
125 130 135	
TTT GCT GTC CGA AGA TAC ATT GAG CAT TAC TTG GAG GAG TTC TTA ATA	546
Phe Ala Val Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe Leu Ile	
140 145 150	
TCT GCA AAT ACA TAC TTC ATG GTT GGC CAC AAA GTC ATC TTT TAC ATC	594
Ser Ala Asn Thr Tyr Phe Met Val Gly His Lys Val Ile Phe Tyr Ile	
155 160 165	
ATG GTG GAT GAT ATC TCC AGG ATG CCT TTG ATA GAG CTG GGT CCT CTG	642
Met Val Asp Asp Ile Ser Arg Met Pro Leu Ile Glu Leu Gly Pro Leu	
170 175 180	
CGT TCC TTT AAA GTG TTT GAG ATC AAG TCC GAG AAG AGG TGG CAA GAC	690
Arg Ser Phe Lys Val Phe Glu Ile Lys Ser Glu Lys Arg Trp Gln Asp	
185 190 195 200	
ATC AGC ATG ATG CGC ATG AAG ACC ATC GGG GAG CAC ATC CTG GCC CAC	738
Ile Ser Met Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His	
205 210 215	
ATC CAG CAC GAG GTG GAC TTC CTC TTC TGC ATG GAC GTG GAT CAG GTC	786
Ile Gln His Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val	
220 225 230	
TTC CAA AAC AAC TTT GGG GTG GAG ACC CTG GGC CAG TCG GTG GCT CAG	834
Phe Gln Asn Asn Phe Gly Val Glu Thr Leu Gly Gln Ser Val Ala Gln	
235 240 245	
CTA CAG GCC TGG TGG TAC AAG GCA CAT CCT GAC GAG TTC ACC TAC GAG	882
Leu Gln Ala Trp Trp Tyr Lys Ala His Pro Asp Glu Phe Thr Tyr Glu	
250 255 260	
AGG CGG AAG GAG TCC GCA GCC TAC ATT CCG TTT GGC CAG GGG GAT TTT	930
Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe	
265 270 275 280	
TAT TAC CAC GCA GCC ATT TTT GGG GGA ACA CCC ACT CAG GTT CTA AAC	978
Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr Pro Thr Gln Val Leu Asn	
285 290 295	
ATC ACT CAG GAG TGC TTC AAG GGA ATC CTC CAG GAC AAG GAA AAT GAC	1026
Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu Gln Asp Lys Glu Asn Asp	
300 305 310	
ATA GAA GCC GAG TGG CAT GAT GAA AGC CAT CTA AAC AAG TAT TTC CTT	1074
Ile Glu Ala Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu	
315 320 325	

CTC AAC AAA CCC ACT AAA ATC TTA TCC CCA GAA TAC TGC TGG GAT TAT Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr 330 335 340	1122
CAT ATA GGC ATG TCT GTG GAT ATT AGG ATT GTC AAG ATA GCT TGG CAG His Ile Gly Met Ser Val Asp Ile Arg Ile Val Lys Ile Ala Trp Gln 345 350 355 360	1170
AAA AAA GAG TAT AAT TTG GTT AGA AAT AAC ATC T GACTTTAAAT Lys Lys Glu Tyr Asn Leu Val Arg Asn Asn Ile 365 370	1214
TGTGCCAGCA GTTTCTGAA TTTGAAAGAG TATTACTCTG GCTACTTCCT CAGAGAAGTA	1274
GCACCTTAATT TTAACCTTTA AAAAAATACT AACAAAATAC CAACACAGTA AGTACATATT	1334
ATTCTTCCTT GCAACTTTGA GCCTGTCAA ATGGGAGAAT GACTCTGTGG TAATCAGATG	1394
TAAATTCCCA GTGATTTC	1412

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGGGGCCG GGCGAGCTG GGAGCGTCGA GCCCGCTGCC CAGCGCCCGC CGGCTCCCTC 60
GCGCCCTGCGC CCGCCGCCCG GGAGGAGCGC CCGGCGGCCG GCGACGGGA GCGCAGCGGC 120
ACACCCCGCC CCGGCACGCC CGCGGGCTC GGGAGGAGGC AGCGCGCCGA CTGTTCCGGC 180
AGCCGAGGAC GCCGCCGGGG AGCCGAGGCG CCGGCCAGCC CCCAGCGCGC CCAGCTTCTG 240
CGGATCAGGG AAACCACGTG TCCTCAAGTG GCCAGCCAGC TGTCCCCAAG AGGAACCTTGC 300
CTGGCATTG CACGGAAAGA CGAGACACTT CACAAAATCA ACGGAGTCAG AAGGCTGCAC 360
CTTCGCTTCC TCCCAGCCCT GCCTCCTTCT GCAGAACGGA GCTCAGTAGA ACTTGGTACT 420
TTTGCCTTT ACTCTAGGAG GAGAGAAGCA GACGATGAGG AGAAAATA ATG AAT GTC 477
Met Asn Val

AAA GGA AAA GTG ATT CTG TCA ATG CTG GTT GTC TCA ACT GTC ATT GTT Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr Val Ile Val 5 10 15	525
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GTG TTT TGG GAA TAT ATC CAC AGC CCA GAA GGC TCT TTG TTC TGG ATA Val Phe Trp Glu Tyr Ile His Ser Pro Glu Gly Ser Leu Phe Trp Ile 20 25 30 35	573
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AAC CCA TCA AGA AAC CCA GAA GTT GGT GGC AGC AGC ATT CAG AAG GGC Asn Pro Ser Arg Asn Pro Glu Val Gly Gly Ser Ser Ile Gln Lys Gly 40 45 50	621
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TGG TGG CTT CCG AGA TGG TTT AAC AAT GGT TAC CAT GAA GAA GAT GGA Trp Trp Leu Pro Arg Trp Phe Asn Asn Gly Tyr His Glu Glu Asp Gly 55 60 65	669
GAC ATA AAC GAA GAA AAG GAA CAA AGA AAC GAA GAC GAA AGC AAG CTT Asp Ile Asn Glu Glu Lys Glu Gln Arg Asn Glu Asp Glu Ser Lys Leu 70 75 80	717
AAG CTA TCG GAC TGG TTC AAC CCA TTT AAA CGC CCC GAG GTT GTG ACC Lys Leu Ser Asp Trp Phe Asn Pro Phe Lys Arg Pro Glu Val Val Thr 85 90 95	765
ATG ACG AAG TGG AAG GCT CCA GTG GTG TGG GAA GGC ACT TAC AAC AGA Met Thr Lys Trp Lys Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Arg 100 105 110 115	813
GCC GTC TTA GAC AAT TAT TAT GCC AAG CAG AAA ATT ACC GTC GGC CTG Ala Val Leu Asp Asn Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu 120 125 130	861
ACG GTT TTC GCC GTC GGA AGA TAC ATT GAG CAT TAC TTG GAG GAG TTC Thr Val Phe Ala Val Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe 135 140 145	909
TTA ACG TCT GCT AAT AAG CAC TTC ATG GTG GGC CAC CCA GTC ATC TTT Leu Thr Ser Ala Asn Lys His Phe Met Val Gly His Pro Val Ile Phe 150 155 160	957
TAT ATC ATG GTA GAT GAT GTC TCC AGG ATG CCT TTG ATA GAG TTG GGT Tyr Ile Met Val Asp Asp Val Ser Arg Met Pro Leu Ile Glu Leu Gly 165 170 175	1005
CCT CTG CGC TCC TTC AAA GTG TTT AAG ATC AAG CCT GAG AAG AGG TGG Pro Leu Arg Ser Phe Val Phe Lys Ile Lys Pro Glu Lys Arg Trp 180 185 190 195	1053
CAG GAC ATC AGC ATG ATG CGC ATG AAG ACT ATC GGG GAG CAC ATT GTG Gln Asp Ile Ser Met Met Arg Met Lys Thr Ile Gly Glu His Ile Val 200 205 210	1101
GCC CAC ATC CAG CAT GAG GTT GAC TTC CTT TTC TGC ATG GAT GTG GAC Ala His Ile Gln His Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp 215 220 225	1149
CAG GTC TTC CAA GAC AAG TTT GGG GTG GAG ACC CTG GGC GAG TCG GTG Gln Val Phe Gln Asp Lys Phe Gly Val Glu Thr Leu Gly Glu Ser Val 230 235 240	1197
GCC CAG CTA CAA GCC TGG TGG TAC AAG GCA GAT CCC AAT GAC TTC ACC Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala Asp Pro Asn Asp Phe Thr 245 250 255	1245
TAC GAG AGG CGG AAG GAG TCT GCA GCA TAC ATT CCC TTC GGC GAA GGG Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro Phe Gly Glu Gly 260 265 270 275	1293
GAT TTT TAT TAC CAT GCA GCC ATT TTT GGG GGA ACA CCC ACT CAG GTC Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr Pro Thr Gln Val 280 285 290	1341

CTT AAC ATC ACC CAG GAA TGC TTC AAA GGA ATC CTC AAG GAC AAG AAA Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu Lys Asp Lys Lys 295 300 305	1389
AAT GAC ATA GAA GCC CAA TGG CAT GAT GAA AGC CAT CTA AAC AAG TAT Asn Asp Ile Glu Ala Gln Trp His Asp Glu Ser His Leu Asn Lys Tyr 310 315 320	1437
TTC CTT CTC AAC AAA CCT ACT AAA ATC TTA TCC CCG GAA TAC TGC TGG Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp 325 330 335	1485
GAT TAT CAC ATA GGC CTA CCT GCG GAT ATT AAG CTT GTC AAG ATG TCT Asp Tyr His Ile Gly Leu Pro Ala Asp Ile Lys Leu Val Lys Met Ser 340 345 350 355	1533
TGG CAG ACA AAA GAG TAT AAT GTG GTT AGA AAT AAT GTC T GACTTTGTGC Trp Gln Thr Lys Glu Tyr Asn Val Val Arg Asn Asn Val 360 365	1583
CAGTACATTT CTGAATTGAGAGTATTAA TTCTGGCTAC TTCCCTCAGAA AAGTAACACT TAATTTAAC TTAAAAAAA ATACTAACAA AAGACCAACA CAGCAAATAC ATATTATTTC TCCTTGTAAC TTTGAGCCTT GTAATACGGG AGAATGAACC TGTGGTAATC AGATGTAAAT TCCCAGTGAT TTCTTACCTA TTTTTGGTTG TGGGGCGGG GAATGGATAC ACCATCAGTT GAACC	1643 1703 1763 1823 1828

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGTCTTAGGA GGCTGGAGAT TCTGGGTGGA GCCCTAGCCC TGCCTTTCT TAGCTGGCTG ACACCTTCCC TTGTAGACTC TTCTTGGAAAT GAGAAGTACC GATTCTGCTG AAGACCTCGC GCTCTAGGC TCTGGGAGTT GGAACCCCTCG TACCTTCCTT TCCTCTGCTG AGCCCTGCCT CCTTCGGCAG GCCAGAGCTG ACAGAAGCTC GGTGCTTG CTGTTGCTT TGGAGGGAAC ACAGCTGACG ATGAGGGCTGA CTTTGAACTC AAGAGATCTG CTTACCCAG TCTCCTGGAA TTAAAAGCCT GTACTACCTT GCCTGGACCT AAGATTTCA TGATCACTAT GCTTCAAGAT CTCCATGTCA ACAAGATCTC CATGTCAAGA TCCAAGTCAG AAACAAGTCT TCCATCCTCA AGATCTGGAT CACAGGAGAA AATA ATG AAT GTC AAG GGA AAA GTA ATC CTG Met Asn Val Lys Gly Lys Val Ile Leu	50 120 180 240 300 360 420 471
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TTG ATG CTG ATT GTC TCA ACC GTG GTT GTC GTG TTT TGG GAA TAT GTC	519
Leu Met Leu Ile Val Ser Thr Val Val Val Val Phe Trp Glu Tyr Val	
10 15 20 25	
AAC AGC CCA GAC GGC TCT TTC TTG TGG ATA TAT CAC ACA AAA ATT CCA	567
Asn Ser Pro Asp Gly Ser Phe Leu Trp Ile Tyr His Thr Lys Ile Pro	
30 35 40	
GAG GTT GGT GAG AAC AGA TGG CAG AAG GAC TGG TGG TTC CCA AGC TGG	615
Glu Val Gly Glu Asn Arg Trp Gln Lys Asp Trp Trp Phe Pro Ser Trp	
45 50 55	
TTT AAA AAT GGG ACC CAC AGT TAT CAA GAA GAC AAC GTA GAA GGA CGG	663
Phe Lys Asn Gly Thr His Ser Tyr Gln Glu Asp Asn Val Glu Gly Arg	
60 65 70	
AGA GAA AAG GGT AGA AAT GGA GAT CGC ATT GAA GAG CCT CAG CTA TGG	711
Arg Glu Lys Gly Arg Asn Gly Asp Arg Ile Glu Glu Pro Gln Leu Trp	
75 80 85	
GAC TGG TTC AAT CCA AAG AAC CGC CCG GAT GTT TTG ACA GTG ACC CCG	759
Asp Trp Phe Asn Pro Lys Asn Arg Pro Asp Val Leu Thr Val Thr Pro	
90 95 100 105	
TGG AAG GCG CCG ATT GTG TGG GAA GGC ACT TAT GAC ACA GCT CTG CTG	807
Trp Lys Ala Pro Ile Val Trp Glu Gly Thr Tyr Asp Thr Ala Leu Leu	
110 115 120	
GAA AAG TAC TAC GCC ACA CAG AAA CTC ACT GTG GGG CTG ACA GTG TTT	855
Glu Lys Tyr Tyr Ala Thr Gln Lys Leu Thr Val Gly Leu Thr Val Phe	
125 130 135	
GCT GTG GGA AAG TAC ATT GAG CAT TAC TTA GAA GAC TTT CTG GAG TCT	903
Ala Val Gly Lys Tyr Ile Glu His Tyr Leu Glu Asp Phe Leu Glu Ser	
140 145 150	
GCT GAC ATG TAC TTC ATG GTT GGC CAT CGG GTC ATA TTT TAC GTC ATG	951
Ala Asp Met Tyr Phe Met Val Gly His Arg Val Ile Phe Tyr Val Met	
155 160 165	
ATA GAT GAC ACC TCC CGG ATG CCT GTC GTG CAC CTG AAC CCT CTA CAT	999
Ile Asp Asp Thr Ser Arg Met Pro Val Val His Leu Asn Pro Leu His	
170 175 180 185	
TCC TTA CAA GTC TTT GAG ATC AGG TCT GAG AAG AGG TGG CAG GAT ATC	1047
Ser Leu Gln Val Phe Glu Ile Arg Ser Glu Lys Arg Trp Gln Asp Ile	
190 195 200	
AGC ATG ATG CGC ATG AAG ACC ATT GGG GAG CAC ATC CTG GCC CAC ATC	1095
Ser Met Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His Ile	
205 210 215	
CAG CAC GAG GTC GAC TTC CTC TTC TGC ATG GAC GTG GAT CAA GTC TTT	1143
Gln His Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val Phe	
220 225 230	
CAA GAC AAC TTC GGG GTG GAA ACT CTG GGC CAG CTG GTA GCA CAG CTC	1191
Gln Asp Asn Phe Gly Val Glu Thr Leu Gly Gln Leu Val Ala Gln Leu	
235 240 245	

CAG ·GCC TGG TGG TAC AAG GCC AGT CCC GAG AAG TTC ACC TAT GAG AGG Gln Ala Trp Trp Tyr Lys Ala Ser Pro Glu Lys Phe Thr Tyr Glu Arg 250 255 260 265	1239
CGG GAA CTG TCG GCC GCG TAC ATT CCA TTC GGA GAG GGG GAT TTT TAC Arg Glu Leu Ser Ala Ala Tyr Ile Pro Phe Gly Glu Gly Asp Phe Tyr 270 275 280	1287
TAC CAC GCG GCC ATT TTT GGA GGA ACG CCT ACT CAC ATT CTC AAC CTC Tyr His Ala Ala Ile Phe Gly Gly Thr Pro Thr His Ile Leu Asn Leu 285 290 295	1335
ACC AGG ·GAG TGC TTT AAG GGG ATC CTC CAG GAC AAG AAA CAT GAC ATA Thr Arg Glu Cys Phe Lys Gly Ile Leu Gln Asp Lys Lys His Asp Ile 300 305 310	1383
GAA GCC CAG TGG CAT GAT GAG AGC CAC CTC AAC AAA TAC TTC CTT TTC Glu Ala Gln Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Phe 315 320 325	1431
AAC AAA CCC ACT AAA ATC CTA TCT CCA GAG TAT TGC TGG GAC TAT CAG Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr Gln 330 335 340 345	1479
ATA GGC CTG CCT TCA GAT ATT AAA AGT GTC AAG GTA GCT TGG CAG ACA Ile Gly Leu Pro Ser Asp Ile Lys Ser Val Lys Val Ala Trp Gln Thr 350 355 360	1527
AAA GAG TAT AAT TTG GTT AGA AAT AAT GTC T GACTTCAAAT TGTGATGGAA Lys Glu Tyr Asn Leu Val Arg Asn Asn Val 365 370	1578
ACTTGACACT ATTACTCTGG CTAATTCTC AAACAAGTAG CAACACTTGA TTTCAACTTT	1638
TAAAAGAAAC AATCAAAACC AAAACCCACT ACCATGGCAA ACAGATGATT TCTCCTGACA	1698
CCTTGAGCCT GTAATATGTG AGAAAGAGTC TATGGCAAGT AATCAGGTAT AAATTCTCAA	1758
TGATTTCTTA TATATTCTGG GTCTTGGAA AACTTGATTC TAGAAATCAA AATTAATTG	1818
ACAAAGGAAA AGCAGATGCC GGAAACTCT TCCCAGTCTG TCATACAATT CACCACTGGC	1878
CAGGTGCTGA GAGAACGATT AGGGAACAGT GTGGGTTGTG TCAGAGTTGG ACGGCTCCAT	1938
CCCTTGGCT TCATTATCFT CCTCCTCATG GAGATTCTAA AGCAACCCAG AGAGGCTTTG	1998
CAGCCAGAGA CCTTTAATAA GGATGCCAAT GTGACCCTCA GTCTGTAAA GCTGATGGCT	2058
CCAGGAGCGC TGGCAGTCCA GGCCCCACTA GGCTATTGTT TCTGTCCTGG GCATAAAGGA	2118
GGCAGAGAGT GCCAATAGGT ACTTTGGTGG CACATGTTCA GAGTCCAGGA AAAATCAAGG	2178
GTGACCACCT AGAGGGACAT AGGACTTGGG GTTGGTGATT GAACTGAGTT ACAAACACAG	2238
ACAGCTTCT TCAGGATGAC TAACAGCAGG AATTGAATGG AAAGTGTGTT CATTTGTGTT	2298
TGCCCAAATT GTATTCATGC TGTTAGCTTT GTGTGTTGAG CCCTGTGGAG AGGGTGTGAC	2358
TGTATCAGGG AAGGAGAGTA CCTCAGCGGA CTGAGGACCA GCACCCCTATT ATATCAGAAG	2418
ACAATCTCTC ATCATCAGGT CCTACCTACA ACCTGCTCTG AACCTCCGAG TTCCTCAGCC	2478

CATGGTGTTC	CAGTGTGGGG	GCCTGTATGG	AGCAGGTGAC	TGAAGACAAA	GCCCCCTGTC	2538
ACATGACCTC	ATTTCCCTG	CTCTAGTACT	ATGCAAGTGT	GACAGCCAGC	CAGCCAGATG	2598
TACTGGACAA	CATAGGAACC	GACTTTATGG	CAATGGGAGC	CGCAGTCACT	ACAAACGGAGC	2658
TGCTGAAGGT	TCTGTTCCCC	GCTCTGAGAG	CCTGCAGGAG	CCCCTGTATA	GGTGGTTCTC	2718
AACCTATGGG	TCGCGACCCC	TTTGGGAAGT	GTTAAATGAC	CCTTTACAG	GTGTCCCCTA	2778
AGACGGTTAA	AAAACATAGA	TATTTCCACT	CTGACTGGTA	ACAGTAGCAG	AATTACAGTT	2838
ATGAAATAGC	AAGGGAAATA	ATTCTGGGTT	TCGTGTCA	CATACCATGA	GGAGCTACAT	2898
TAGGTACACAT	CATTAGGGAA	GTTGAGAAGC	ATAGCTCTAC	TTGGGTATTT	AAGCAAATTA	2958
TGCAAAGGGG	GTTGTCGCTC	TGTGTTCTGT	GTATGCATAT	ATTTATATTT	TGCTTGTCTT	3018
CCAGTTAGG	TCAATCTGTT	TCTTCCTTTA	AGCAGTTAT	TTAAAAGGCC	ATTGCACCAT	3078
CTTGGTGAAC	AGCATGAGGG	GTTCATAAA	AAAATAGGAT	CTTACCTTG	TCCACAGGGC	3138
TCTACCTCTT	ACTTTCAAT	TGTGAACAAA	AAAGGTCGCA	CACCCAGAGG	CAACAAAACC	3198
CACAGAATTC	CTGAACCAAT	GGGAGATGCC	AATGGAAGCA	GAGCTTGCAC	ATCTGCTAAA	3258
AATTCTGCCT	CTCTGTCACT	GTGCTGGATC	CGTCTAAAGT	GGGACAGTTC	AATGGTCTGA	3318
AAGTTTCAA	AAGGCTGGGG	AATTTGAGGG	GATTTTTTTT	TAAAATAAAA	TTGATCCAAG	3378
TTTAAATCTC	TAATGAGTAA	GCTTAGGATT	TTATTAAAGG	TAATTTTAG	ACATTCTTCA	3438
AAATAAGAAT	TC					3450

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asn	Val	Lys	Gly	Arg	Val	Val	Leu	Ser	Met	Leu	Leu	Val	Ser	Thr
1						5				10					15

Val	Met	Val	Val	Phe	Trp	Glu	Tyr	Ile	Asn	Ser	Pro	Glu	Gly	Ser	Leu
						20			25					30	

Phe	Trp	Ile	Tyr	Gln	Ser	Lys	Asn	Pro	Glu	Val	Gly	Ser	Ser	Ala	Gln
						35			40				45		

Arg	Gly	Trp	Trp	Phe	Pro	Ser	Trp	Phe	Asn	Asn	Gly	Thr	His	Ser	Tyr
						50			55			60			

His	Glu	Glu	Glu	Asp	Ala	Ile	Gly	Asn	Glu	Lys	Glu	Gln	Arg	Lys	Glu
						65			70			75			80

Asp	Asn	Arg	Gly	Glu	Leu	Pro	Leu	Val	Asp	Trp	Phe	Asn	Pro	Glu	Lys
									85			90			95

Arg Pro Glu Val Val Thr Ile Thr Arg Trp Lys Ala Pro Val Val Trp
 100 105 110
 Glu Gly Thr Tyr Asn Arg Ala Val Leu Asp Asn Tyr Tyr Ala Lys Gln
 115 120 125
 Lys Ile Thr Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr Ile Glu
 130 135 140
 His Tyr Leu Glu Glu Phe Leu Ile Ser Ala Asn Thr Tyr Phe Met Val
 145 150 155 160
 Gly His Lys Val Ile Phe Tyr Ile Met Val Asp Asp Ile Ser Arg Met
 165 170 175
 Pro Leu Ile Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe Glu Ile
 180 185 190
 Lys Ser Glu Lys Arg Trp Gln Asp Ile Ser Met Met Arg Met Lys Thr
 195 200 205
 Ile Gly Glu His Ile Leu Ala His Ile Gln His Glu Val Asp Phe Leu
 210 215 220
 Phe Cys Met Asp Val Asp Gln Val Phe Gln Asn Asn Phe Gly Val Glu
 225 230 235 240
 Thr Leu Gly Gln Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala
 245 250 255
 His Pro Asp Glu Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr
 260 265 270
 Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly
 275 280 285
 Gly Thr Pro Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly
 290 295 300
 Ile Leu Gln Asp Lys Glu Asn Asp Ile Glu Ala Glu Trp His Asp Glu
 305 310 315 320
 Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu
 325 330 335
 Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly Met Ser Val Asp Ile
 340 345 350
 Arg Ile Val Lys Ile Ala Trp Gln Lys Lys Glu Tyr Asn Leu Val Arg
 355 360 365
 Asn Asn Ile
 370

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr
 1 5 10 15

Val Ile Val Val Phe Trp Glu Tyr Ile His Ser Pro Glu Gly Ser Leu
 20 25 30

Phe Trp Ile Asn Pro Ser Arg Asn Pro Glu Val Gly Gly Ser Ser Ile
 35 40 45

Gln Lys Gly Trp Trp Leu Pro Arg Trp Phe Asn Asn Gly Tyr His Glu
 50 55 60

Glu Asp Gly Asp Ile Asn Glu Glu Lys Glu Gln Arg Asn Glu Asp Glu
 65 70 75 80

Ser Lys Leu Lys Leu Ser Asp Trp Phe Asn Pro Phe Lys Arg Pro Glu
 85 90 95

Val Val Thr Met Thr Lys Trp Lys Ala Pro Val Val Trp Glu Gly Thr
 100 105 110

Tyr Asn Arg Ala Val Leu Asp Asn Tyr Tyr Ala Lys Gln Lys Ile Thr
 115 120 125

Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr Ile Glu His Tyr Leu
 130 135 140

Glu Glu Phe Leu Thr Ser Ala Asn Lys His Phe Met Val Gly His Pro
 145 150 155 160

Val Ile Phe Tyr Ile Met Val Asp Asp Val Ser Arg Met Pro Leu Ile
 165 170 175

Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe Lys Ile Lys Pro Glu
 180 185 190

Lys Arg Trp Gln Asp Ile Ser Met Met Arg Met Lys Thr Ile Gly Glu
 195 200 205

His Ile Val Ala His Ile Gln His Glu Val Asp Phe Leu Phe Cys Met
 210 215 220

Asp Val Asp Gln Val Phe Gln Asp Lys Phe Gly Val Glu Thr Leu Gly
 225 230 235 240

Glu Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala Asp Pro Asn
 245 250 255

Asp Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro Phe
 260 265 270

Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr Pro
 275 280 285

Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu Lys
 290 295 300

Asp Lys Lys Asn Asp Ile Glu Ala Gln Trp His Asp Glu Ser His Leu
 305 310 315 320

Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro Glu
 325 330 335

Tyr Cys Trp Asp Tyr His Ile Gly Leu Pro Ala Asp Ile Lys Leu Val
 340 345 350

Lys Met Ser Trp Gln Thr Lys Glu Tyr Asn Val Val Arg Asn Asn Val
 355 360 365

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asn Val Lys Gly Lys Val Ile Leu Leu Met Leu Ile Val Ser Thr
 1 5 10 15

Val Val Val Val Phe Trp Glu Tyr Val Asn Ser Pro Asp Gly Ser Phe
 20 25 30

Leu Trp Ile Tyr His Thr Lys Ile Pro Glu Val Gly Glu Asn Arg Trp
 35 40 45

Gln Lys Asp Trp Trp Phe Pro Ser Trp Phe Lys Asn Gly Thr His Ser
 50 55 60

Tyr Gln Glu Asp Asn Val Glu Gly Arg Arg Glu Lys Gly Arg Asn Gly
 65 70 75 80

Asp Arg Ile Glu Glu Pro Gln Leu Trp Asp Trp Phe Asn Pro Lys Asn
 85 90 95

Arg Pro Asp Val Leu Thr Val Thr Pro Trp Lys Ala Pro Ile Val Trp
 100 105 110

Glu Gly Thr Tyr Asp Thr Ala Leu Leu Glu Lys Tyr Tyr Ala Thr Gln
 115 120 125

Lys Leu Thr Val Gly Leu Thr Val Phe Ala Val Gly Lys Tyr Ile Glu
 130 135 140

His Tyr Leu Glu Asp Phe Leu Glu Ser Ala Asp Met Tyr Phe Met Val
 145 150 155 160

Gly His Arg Val Ile Phe Tyr Val Met Ile Asp Asp Thr Ser Arg Met
 165 170 175

Pro Val Val His Leu Asn Pro Leu His Ser Leu Gln Val Phe Glu Ile
 180 185 190

Arg Ser Glu Lys Arg Trp Gln Asp Ile Ser Met Met Arg Met Lys Thr
 195 200 205

Ile Gly Glu His Ile Leu Ala His Ile Gln His Glu Val Asp Phe Leu
 210 215 220

Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp Asn Phe Gly Val Glu
 225 230 235 240

Thr Leu Gly Gln Leu Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala
 245 250 255

Ser Pro Glu Lys Phe Thr Tyr Glu Arg Arg Glu Leu Ser Ala Ala Tyr
 260 265 270

Ile Pro Phe Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly
 275 280 285

Gly Thr Pro Thr His Ile Leu Asn Leu Thr Arg Glu Cys Phe Lys Gly
 290 295 300

Ile Leu Gln Asp Lys Lys His Asp Ile Glu Ala Gln Trp His Asp Glu
 305 310 315 320

Ser His Leu Asn Lys Tyr Phe Leu Phe Asn Lys Pro Thr Lys Ile Leu
 325 330 335

Ser Pro Glu Tyr Cys Trp Asp Tyr Gln Ile Gly Leu Pro Ser Asp Ile
 340 345 350

Lys Ser Val Lys Val Ala Trp Gln Thr Lys Glu Tyr Asn Leu Val Arg
 355 360 365

Asn Asn Val
 370

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGGGCTGCA GGAATTCGAT GATCCCCAG CTTGAAGTTC CTATTCCGAA GTTCCTATT	60
TCTAGAAAGT ATAGGAACCTT GAAGCTGGC TGCAGGAATT CGATTCTGAGC AGTGTGGTT	120
TGCAAGAGGA AGCAAAAAGC CTCTCCACCC AGGCCTGGAA TGTTTCCACC CAATGTCGAG	180
CAGTGTGGTT TTGCAAGAGG AAGCAAAAAG CCTCTCCACC CAGGCCTGGA ATGTTCCAC	240
CCAATGTCGA GCAAACCCCG CCCAGCGTCT TGTCAATTGGC GAATTGAAAC ACCGAGATGC	300
AGTCGGGGCG GCGCGGTCCC AGGTCCACTT GGCATATTAA GGTGACCGGT GTGGCCTCGA	360
ACACCGAGCG ACCCTGCAGC CAATATGGGA TCGGCCATTG AACAAAGATGG ATTGCACGCA	420
GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA TTGGCTATG ACTGGGCACA ACAGACAATC	480
GGCTGCTCTG ATGCCGCCGT GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTGTC	540

AAGACCGACC	TGTCCGGTGC	CCTGAATGAA	CTCCAAGACG	AGGCAGCGCG	GCTATCGTGG	600
CTGGCCACGA	CGGGCGTTCC	TTGCGCAGCT	GTGCTCGACG	TTGTCACTGA	TGCGGGAAAGG	660
GAATGGCTGC	TATTGGGCAGA	AGTGCCGGGG	CAGGATCTCC	TGTCATCTCA	CCTTGCTCCT	720
GCGGAGAAAG	TATCCATCAT	GGCTGATGCA	ATGCGGCGGC	TGCATAACGCT	TGATCCGGCT	780
ACCTGCCCCAT	TCGACCACCA	AGCGAAACAT	CGCATCGAGC	GAGCACGTAC	TCGGATGGAA	840
GCGGGCTTG	TCGATCAGGA	TGATCTGGAC	GAAGAGCATC	AGGGGCTCGC	GCCAGCCGAA	900
CTGTTCGCCA	GGCTCAAGGC	GCGGATGCC	GACGGCGAGG	ATCTCGTCGT	GACCCATGGC	960
GATGCCTGCT	TGCCGAATAT	CATGGTGGAA	AATGGCCGCT	TTTCTGGATT	CATCGACTGT	1020
GGCCGGCTGG	GTGTGGCGGA	CCGCTATCAG	GACATAGCGT	TGGCTACCCG	TGATATTGCT	1080
GAAGAGCTTG	GCGGCGAATG	GGCTGACCGC	TTCCTCGTGC	TTTACGGTAT	CGCCGCTCCC	1140
GATTGCGAGC	GCATCGCCTT	CTATGCCCTT	CTTGACGAGT	TCTTCTGAGG	GGATCGGCAA	1200
TAAAAAGACA	GAATAAAACG	CACGGGTGTT	GGCGTTTGT	TCGGATCATC	AAGCTTGAAG	1260
TTCCTATTCC	GAAGTTCCTA	TTCTCTAGAA	AGTATAGGAA	CTTCAAGCTT	ATCGATGAGT	1320
AGATCTTGAT	CGATACCGTC					1340

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTGGAAAA GTACTACGCC ACACAGAAAC TCA

33

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCCAGAGTA ATAGTGTCAA GTTTCCATCA CAA

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCACACGCG TCACCTTAAT AATATGCCAA GTGGAC

36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCAGCATGAT GCGCATGAAG AC

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGCCGCGTG GTAGTAAAAA

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGACGAG TTCTTCTGAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGAGATCGC ATTGAAGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGCCGCGTG GTAGTAAAAA

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGTTTTGGT TTTGATTGTT

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGAATTCAT GTTAAACATG GGAGGCC

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGAATTCTG CCCACTCCCT GCCGATG

27

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTGACACCTT TCGCTTCCT CTTGCGTGT CGCCTGCGAC CTTTCCCCAC CCCGGCCTCT

60

TTCCTGGTTG CACCACTTCC TCTCATTCCA AAGGATTGTG CCCTTACTGC TGCTGGTTCT

120

GCACTGGAAA CACGGGGCAG GGAGCCCTCT TCCCATCACC CCTGTAAATG CCACCTGTGC

180

CATACGCCAC CCATGCCACG GCAACCTC ATG AAC CAG ATC AAG AAT CAA CTG
Met Asn Gln Ile Lys Asn Gln Leu

232

375

GCA CAG CTC AAT GGC AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA
Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr
380 385 390 395

280

GCT CAA GGG GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT
Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro
400 405 410

328

AAC ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG ACC
Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys Thr
415 420 425

376

AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC GCC TCC CTG	424
Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser Ala Ser Leu	
430 435 440	
ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC CCC ACT GCC GTG AGC	472
Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn Pro Thr Ala Val Ser	
445 450 455	
CTC CAG GTC AAG CTC AAT GCT ACT ATA GAC GTC ATG AGG GGC CTC CTC	520
Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val Met Arg Gly Leu Leu	
460 465 470 475	
AGC AAT GTG CTT TGC CGT CTG TGC AAC AAG TAC CGT GTG GGC CAC GTG	568
Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr Arg Val Gly His Val	
480 485 490	
GAT GTG CCA CCT GTC CCC GAC CAC TCT GAC AAA GAA GCC TTC CAA AGG	616
Asp Val Pro Pro Val Pro Asp His Ser Asp Lys Glu Ala Phe Gln Arg	
495 500 505	
AAA AAG TTG GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT	664
Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser	
510 515 520	
GTG GTG GTC CAG GCC TTC T AGAGAGGAGG TCTTGAATGT ACCATGGACT	713
Val Val Val Gln Ala Phe	
525	

G

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn	
1 5 10 15	
Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn	
20 25 30	
Asn Val Glu Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe	
35 40 45	
His Gly Asn Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met	
50 55 60	
Val Ala Tyr Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys	
65 70 75 80	
Val Leu Asn Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr	
85 90 95	

Ile Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys
 100 105 110

Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His
 115 120 125

Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu
 130 135 140

Gly Thr Tyr Lys Gln Val Ile Ser Val Val Val Gln Ala Phe
 145 150 155

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACACGGTACT TGTTGCA

17

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCTGGTCCC GGGTGATATT GGTCA

25

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCATGGCCTC GAGGGCCCCC CCCCCCCCC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCTTTCGC TTTCCT

16

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACCTTTGCTTTCTCTGCA CCATTTCTCTC TCCCTCCCTG AGCCGGAGTT

60

GTGCCCTGCTGTTGGTTCTGCACATGGAAAATGGGGCGGGAGCCCCCTCCCCATCACCG

120

CCTGTCAACG CCACCTGTGC CATA CGCCAC CCAT GTCACA ACAACCTC ATG AAC CAG
Met Asn Gln
160

177

ATC AGG AGC CAA CTG GCA CAG CTC AAT GGC AGT GCC AAT GCC CTC TTT
 Ile Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe
 165 170 175

225

ATT CTC TAT TAC ACA GCC CAG GGG GAG CCG TTC CCC AAC AAC CTG GAC
 Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Leu Asp
 180 185 190

273

AAG CTA TGT GGC CCC AAC GTG ACG GAC TTC CCG CCC TTC CAC GCC AAC
 Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro Pro Phe His Ala Asn
 185 . . . 200 . . . 205

321

GGC ACG GAG AAG GCC AAG CTG GTG GAG CTG TAC CGC ATA GTC GTG TAC
 Gly Thr Glu Lys Ala Lys Leu Val Glu Leu Tyr Arg Ile Val Val Tyr
 210 215 220 225

369

CTT GGC ACC TCC CTG GGC AAC ATC ACC CGG GAC CAG AAG ATC CTC AAC
 Leu Gly Thr Ser Leu Gly Asn Ile Thr Arg Asp Gln Lys Ile Leu Asn
 210 225 240

417

CCC AGT GCC CTC AGC CTC CAC AGC AAG CTC AAC GCC ACC GCC GAC ATC
 Pro Ser Ala Leu Ser Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile
 315 350 355

465

CTG CGA GGC CTC CTT AGC AAC GTG CTG TGC CGC CTG TGC AGC AAG TAC
 Leu Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr
 266 265 270

CAC GTG GGC CAT GTG GAC GTG ACC TAC GGC CCT GAC ACC TCG GGT AAG	561
His Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly Lys	
275 280 285	
GAT GTC TTC CAG AAG AAG CTG GGC TGT CAA CTC CTG GGG AAG TAT	609
Asp Val Phe Gln Lys Lys Leu Gly Cys Gln Leu Leu Gly Lys Tyr	
290 295 300 305	
AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC T AGCAGGAGGT	653
Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe	
310 315	

CT 655

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Asn Gln Ile Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn	
1 5 10 15	
Ala Leu Phe Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn	
20 25 30	
Asn Leu Asp Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro Pro Phe	
35 40 45	
His Ala Asn Gly Thr Glu Lys Ala Lys Leu Val Glu Leu Tyr Arg Ile	
50 55 60	
Val Val Tyr Leu Gly Thr Ser Leu Gly Asn Ile Thr Arg Asp Gln Lys	
65 70 75 80	
Ile Leu Asn Pro Ser Ala Leu Ser Leu His Ser Lys Leu Asn Ala Thr	
85 90 95	
Ala Asp Ile Leu Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys	
100 105 110	
Ser Lys Tyr His Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr	
115 120 125	
Ser Gly Lys Asp Val Phe Gln Lys Lys Leu Gly Cys Gln Leu Leu	
130 135 140	
Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe	
145 150 155	

(2). INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGTTGGTTC TGCACGTGGA